

distinguish one individual from another, even across multiple health plans. In developing this longitudinal dataset, a series of administrative and technical issues were addressed—the evaluation of claims data as proxies for evaluating clinical measures, methods for standardizing data from multiple sources, the identification of providers from multiple data sources and with multiple identifiers, building time-horizons and data integrity checks that work across the disparate data sources. **RESULTS:** Strong Square, LLC has datasets that contain masked patient-specific data and unique provider identification that allows for tracking a patient's utilization of antibiotic prescriptions over time and over multiple health plans. **CONCLUSIONS:** This project provided physicians with a single, unified reporting mechanism that measures each physician's antibiotic prescribing patterns. Because of the data methods, tools and processes developed for this initiative, we are reporting a complete “picture” of physician antibiotic prescribing patterns across all major health care payors in the State of Washington over time without revealing patient-identity.

PMD8

PREDICTORS OF ANTIBIOTIC PRESCRIBING FOR UPPER RESPIRATORY INFECTIONS IN AN AMBULATORY POPULATION

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OBJECTIVES: Inappropriate use of antibiotics is now a well documented international health issue with implications for cost of care and antibiotic resistance. The objective of this study is to estimate the probability of receiving an antibiotic for an “inappropriate” diagnosis. Prescribing behavior, in general, has been the subject of research in many countries, but predictors of antibiotic prescribing have received little attention. **METHODS:** South Carolina Medicaid paid claims for 1996 to 2000 are used to estimate probabilities of receiving an antibiotic prescription for an upper respiratory infection (URI). Patient variables include demographics (age, race, gender, urban/rural location), URI history, ambulatory-service history, and hospital-use history, and URI diagnosis. Prescriber variables include practice load, URI patient mix, and practice specialty), and urban/rural location of practice. Probit analysis is used to estimate the probability of receiving an antibiotic prescription for a viral URI diagnosis. Year of service is included with the above variables to estimate a full-model. **RESULTS:** Probability estimates indicate that the most likely recipient of an antibiotic for a viral URI was female (0.270), non-white (0.269), and age 5 to 18 year old (0.326). Among prescribers the probability was highest for generalists (0.354), and pediatricians had a probability of 0.226. Overall, from 1996 to 2000, the rate of antibiotic prescribing for viral URIs decreased from 39% to 27%. Shifts in antibiotic use patterns also were observed with amoxicillin being the most frequently used drug in 1996 at 42%. Amoxicillin main-

tained its dominant position over the study period but newer antibiotics increased their share of total utilization. **CONCLUSIONS:** There was a general decline in antibiotic use from 1996 to 2000, but the rate of antibiotic prescribing for viral URIs remains high. The methods employed to track antibiotic use offer a relatively inexpensive approach to identifying and tracking potentially inappropriate prescribing.

PMD9

OPTIMIZATION OF AIDS PILOT CLINICAL TRIAL USING LEAMSIM

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The possibility of performing complete simulations of clinical trials, based on pharmacological action models, has been considered since the advent of the computer era, as a tool to optimise their practical realisation. Thanks to the advances in computation technology and in discrete event simulation tools, today it is possible to perform realistic, large-scale clinical trial simulations in a regular basis using suitable simulation tools. **OBJECTIVES:** We illustrate the process of use the realistic simulator LeanSim, previously for the concrete case of pilot clinical trials devoted to testing efficacy of the antiretroviral didanosine in a group of 50 patients with virologic failure presenting different mutations in the gen of HIV reverse transcriptase. It can origin resistance to transcriptase inhibitors and it can affects the efficacy of treatment designed to reduce the viral load in AIDS patients. **METHODS:** LeanSim is basically a discrete simulation tool developed in C/C++ that can be applied in any ambit, but accepts personalised elements construction, in order to adapt the simulation model to the reality that want to be simulated (this is the lean simulation metaphor). Other important LeanSim aspect is the way in which the model is constructed, this is, via the process definition, which is closer to the clinical trials experiment definition. **RESULTS:** LeanSim allow the population variability simulation (inter/intra patients) and its low cost let general use extend during optimisation previously the clinical trial starts. **CONCLUSIONS:** A simulation model based in Linear Mixed Models was estimated and during the simulation various scenarios were simulated to optimise sample size, effect of missing values, number of centres recruiting patients and the variability inter/intra patients and the previous results indicate the advantages of use this new tool.

PMD10

GENETIC TESTING, PREDICTIVE GENETIC TESTING FOR HEREDITARY CANCER

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